SEQUENCE LISTING

<110> Ingram, L et al.

<120> METHODS AND COMPOSITIONS FOR SIMULTANEOUS
      SACCHARIFICATION AND FERMENTATION

<130> BCI-024CP

<140>
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<150> 60/214,137
<151> 2000-06-26

<150> 60/219,913
<151> 2000-07-21

<160> 17

<170> PatentIn Ver. 2.0

<210> 1
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<213> Zymomonas mobilis

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ggtgttgtta ccttgccgaa gggcaccggt aaaaatgttc gcgtcggtgt tttcgcccgt 180

ggcccgaaag ctgaagaagc taaagctgct ggtgcagaag ttgtcggcgc agaagacctg 240

atggaagcca ttcagggcgg cagcattgat ttcgatcgtg atgccctttta tactgaaatt 300

gccttgcgct gccataatga agcagcctcc ggtgtttttgg cagatttaag cgctgcctga 360

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<213> Zymomonas mobilis

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<223> expression
      vector

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aataccggca ttctgattac aggccgtgtt ttgaatgcgg tatgcagttt tgtctatgtc 120

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tttgctaccc tgatttcgga tattacccgt tttcagtcat ggcaaacctt gctgcattac 240

ggttcaaaag cttttcagga aaaagatttt aaccaatttg atgatgtcct tgccttttgc 300

atcagagccg attttttttag tgcggcgata ggtatgttgg tagggttagg cggtatcttg 360

attttaggca cttcaagatt gggatggcct gccgaggtca agccagatgc cttgctttgt 420

atgctgatta tacttttttat gaatatcggc tggtccaacc gggatgttgc ggctgtgtaa 480

ccgctttaaa ctggtcacta tttatgagtt tattacgacc tgcgtcagaa ccggaggttg 540

tggcattggt tattggcttc atatgccttt ggggtatttt ttgtttatat ggtgcctgac 600

gcaattcacg cttttttgtca cctgtagtta cgctggcatt tatctctttc accaatatac 660

ggagcgagca tttccgataa gaaaaatatt tcagagaaaa acgcccgttg aagggatgtg 720

gaaattcact ttaagcgtca gttttaatga aatcctagac tccattttcc agcagggtgg 780

caccccttgct attggtagct cactgggggc tggggaagcc gctgtctatc gggtcgcgcg 840

ccagattagt aacggtttat ccaaaccagc acagatgatg atcggctaac atgcatccac 900

cggcagcacc ggccgtttta tgcttgggat tattgatatg ccgaaaagga tacaacatct 960

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gcgccatcag ggaatgaaaa atcaatccgt cttttttcggc atgagcaacc aacattttca 1080

aggtatcatc ctgatgcgca atatcggcat cggttagcca taaccatttt acctgtccgg 1140

cggccttaat accttgatca gatggttcgt ggtgttgtta ccttgccgaa gggcaccggt 1200

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<210> 3
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<213> Escherichia coli

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<210> 4
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<212> DNA
<213> Escherichia coli

<220>
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<210> 5
<211> 27
<212> DNA
<213> Escherichia coli

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<223> Description of Artificial Sequence:primer

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<210> 6
<211> 30
<212> DNA
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<210> 7
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<212> DNA
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<223> Description of Artificial Sequence:primer

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<210> 8
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<210> 9
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<212> DNA
<213> Artificial Sequence

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<210> 10
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<212> DNA
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<223> Description of Artificial Sequence:primer

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<210> 11
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<212> DNA
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<223> Description of Artificial Sequence:vector

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<223> all occurrences of n to be sequenced

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<223> nucleotide positions 1-1451 ecodes promoter

<220>
<223> nucleotide positions 1452-2735 encodes celZ gene

<220>
<223> nucleotide positions 4916-5776 encodes bla gene

<220>
<223> nucleotide positions 7061-8251 encodes tet gene

<220>
<223> nucleotide positions 9476-11544 encodes target sequence from K. oxytoca

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<222> (1452)..(2735)

<220>
<221> CDS
<222> (4916)..(5776)

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<221> CDS
<222> (7061)..(8251)

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gcatggacat cccagacatt gggattgaac ctgtttggtg tcatgctttt gattacgact 180

tttgctaccc tgatttcgga tattacccgt tttcagtcat ggcaaacctt gctgcattac 240

ggttcaaaag cttttcagga aaaagatttt aaccaatttg atgatgtcct tgccttttgc 300

atcagagccg attttttttag tgcggcgata ggtatgttgg tagggttagg cggtatcttg 360

attttaggca cttcaagatt gggatggcct gccgaggtca agccagatgc cttgctttgt 420

atgctgatta tacttttat gaatatcggc tggtccaacc gggatgttgc ggctgtgtaa 480

ccgctttaaa ctggtcacta tttatgagtt tattacgacc tgcgtcagaa ccggaggttg 540

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gcaattcacg ctttttgtca cctgtagtta cgctggcatt tatctctttc accaatatac 660

ggagcgagca tttccgataa gaaaaatatt tcagagaaaa acgcccgttg aagggatgtg 720

gaaattcact ttaagcgtca gttttaatga aatcctagac tccattttcc agcagggtgg 780

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ttcgatcgtg atgccctta tactgaaatt gccttgcgct gccataatga agcagcctcc 1380

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gagattcatt t atg cct ctc tct tat tcg gat aac cat cca gtc atc gat   1490
             Met Pro Leu Ser Tyr Ser Asp Asn His Pro Val Ile Asp
              1               5                   10

agc caa aaa cac gcc cca cgt aaa aaa ctg ttt cta tct tgt gcc tgt   1538
Ser Gln Lys His Ala Pro Arg Lys Lys Leu Phe Leu Ser Cys Ala Cys
     15                  20                  25

tta gga tta agc ctt gcc tgc ctt tcc agt aat gcc tgg gcg agt gtt   1586
Leu Gly Leu Ser Leu Ala Cys Leu Ser Ser Asn Ala Trp Ala Ser Val
 30                  35                  40                  45

gag ccg tta tcc gtt agc ggc aat aaa atc tac gca ggt gaa aaa gcc   1634
Glu Pro Leu Ser Val Ser Gly Asn Lys Ile Tyr Ala Gly Glu Lys Ala
                 50                  55                  60

aaa agt ttt gcc ggc aac agc tta ttc tgg agt aat aat ggt tgg ggt   1682
Lys Ser Phe Ala Gly Asn Ser Leu Phe Trp Ser Asn Asn Gly Trp Gly
             65                  70                  75

ggg gaa aaa ttc tac aca gcc gat acc gtt gcg tcg ctg aaa aaa gac   1730
Gly Glu Lys Phe Tyr Thr Ala Asp Thr Val Ala Ser Leu Lys Lys Asp
         80                  85                  90

tgg aaa tcc agc att gtt cgc gcc gct atg ggc gtt cag gaa agc ggt   1778
Trp Lys Ser Ser Ile Val Arg Ala Ala Met Gly Val Gln Glu Ser Gly
     95                  100                 105

ggt tat ctg cag gac ccg gct ggc aac aag gcc aaa gtt gaa aga gtg   1826
Gly Tyr Leu Gln Asp Pro Ala Gly Asn Lys Ala Lys Val Glu Arg Val
110                 115                 120                 125

gtg gat gcc gca atc gcc aac gat atg tat gtg att att gac tgg cac   1874
Val Asp Ala Ala Ile Ala Asn Asp Met Tyr Val Ile Ile Asp Trp His
                 130                 135                 140

tca cat tct gca gaa aac aat cgc agt gaa gcc att cgc ttc ttc cag   1922
Ser His Ser Ala Glu Asn Asn Arg Ser Glu Ala Ile Arg Phe Phe Gln
             145                 150                 155

gaa atg gcg cgc aaa tat ggc aac aag ccg aat gtc att tat gaa atc   1970
Glu Met Ala Arg Lys Tyr Gly Asn Lys Pro Asn Val Ile Tyr Glu Ile
             160                 165                 170

tac aac gag ccg ctt cag gtt tca tgg agc aat acc att aaa cct tat   2018
Tyr Asn Glu Pro Leu Gln Val Ser Trp Ser Asn Thr Ile Lys Pro Tyr
     175                 180                 185

gcc gaa gcc gtg att tcc gcc att cgc gcc att gac ccg gat aac ctg   2066
Ala Glu Ala Val Ile Ser Ala Ile Arg Ala Ile Asp Pro Asp Asn Leu
190                 195                 200                 205

att att gtc ggt acg ccc agt tgg tcg caa aac gtt gat gaa gcg tcg   2114
Ile Ile Val Gly Thr Pro Ser Trp Ser Gln Asn Val Asp Glu Ala Ser
                 210                 215                 220

cgc gat cca atc aac gcc aag aat atc gcc tat acg ctg cat ttc tac   2162
Arg Asp Pro Ile Asn Ala Lys Asn Ile Ala Tyr Thr Leu His Phe Tyr
             225                 230                 235
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gcg gga acc cat ggt gag tca tta cgc act aaa gcc cgc cag gcg tta   2210
Ala Gly Thr His Gly Glu Ser Leu Arg Thr Lys Ala Arg Gln Ala Leu
        240             245             250

aat aac ggt att gcg ctt ttc gtc acc gag tgg ggc gcc gtt aac gcg   2258
Asn Asn Gly Ile Ala Leu Phe Val Thr Glu Trp Gly Ala Val Asn Ala
        255             260             265

gac ggc aat ggc gga gtg aac cag aca gat acc gac gcc tgg gta acg   2306
Asp Gly Asn Gly Gly Val Asn Gln Thr Asp Thr Asp Ala Trp Val Thr
270             275             280             285

ttc atg cgt gac aac aac atc agc aac gca aac tgg gcg tta aat gat   2354
Phe Met Arg Asp Asn Asn Ile Ser Asn Ala Asn Trp Ala Leu Asn Asp
            290             295             300

aaa agc gaa ggg gca tca acc tat tat ccg gac tct aaa aac ctg acc   2402
Lys Ser Glu Gly Ala Ser Thr Tyr Tyr Pro Asp Ser Lys Asn Leu Thr
            305             310             315

gag tcg ggt aaa ata gta aaa tcg atc att caa agc tgg cca tat aaa   2450
Glu Ser Gly Lys Ile Val Lys Ser Ile Ile Gln Ser Trp Pro Tyr Lys
            320             325             330

gcg ggc agc gcc gcc agt aca aca acc gat cag tca acc gat acc acc   2498
Ala Gly Ser Ala Ala Ser Thr Thr Thr Asp Gln Ser Thr Asp Thr Thr
            335             340             345

atg gca cca ccg ttg acg aac cga cca caa ccg aca cac cgg caa acc   2546
Met Ala Pro Pro Leu Thr Asn Arg Pro Gln Pro Thr His Arg Gln Thr
350             355             360             365

gct gat tgc tgc aat gcc aac gtt tac ccc aac tgg gtt agc aaa gac   2594
Ala Asp Cys Cys Asn Ala Asn Val Tyr Pro Asn Trp Val Ser Lys Asp
            370             375             380

tgg gcg ggc cgg cag cga ctc ata acg aag cag gcc aat cga tcg tct   2642
Trp Ala Gly Arg Gln Arg Leu Ile Thr Lys Gln Ala Asn Arg Ser Ser
            385             390             395

aca aag gga acc tgt ata ccg caa act ggt aca ctt cat ccg ttc cgg   2690
Thr Lys Gly Thr Cys Ile Pro Gln Thr Gly Thr Leu His Pro Phe Arg
            400             405             410

gca gcg att cct cct ggg cac agg ttg gta gct gta act aat tga       2735
Ala Ala Ile Pro Pro Gly His Arg Leu Val Ala Val Thr Asn
            415             420             425

ttaatctttt cacccccaaa ataacagggc tgcgattgca gcctgatacg caacattcca 2795

ttacttaatt gcgttcaaaa gcgcccaaat ccggtgcgct gccttgtaac taatatgatt 2855

tctctttcgt acccgcgtta atcagctttg agttagccga cagacggaac agcgaggttg 2915

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cgcgctnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 3335

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nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn nnnnnnnnnn 4235

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tctaaataca ttcaaatatg tatccgctca tgagacaata accctgataa atgcttcaat 4895

aatattgaaa aaggaagagt atg agt att caa cat ttc cgt gtc gcc ctt att 4948
                       Met Ser Ile Gln His Phe Arg Val Ala Leu Ile
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                                    1   10

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ccc ttt ttt gcg gca ttt tgc ctt cct gtt ttt gct cac cca gaa acg    4996
Pro Phe Phe Ala Ala Phe Cys Leu Pro Val Phe Ala His Pro Glu Thr
                               20

ctg gtg aaa gta aaa gat gct gaa gat cag ttg ggt gca cga gtg ggt    5044
Leu Val Lys Val Lys Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly
        30                                       40

tac atc gaa ctg gat ctc aac agc ggt aag atc ctt gag agt ttt cgc    5092
Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg
                       50

ccc gaa gaa cgt ttt cca atg atg agc act ttt aaa gtt ctg cta tgt    5140
Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys
 60                                      70

ggc gcg gta tta tcc cgt att gac gcc ggg caa gag caa ctc ggt cgc    5188
Gly Ala Val Leu Ser Arg Ile Asp Ala Gly Gln Glu Gln Leu Gly Arg
                   80                                        90

cgc ata cac tat tct cag aat gac ttg gtt gag tac tca cca gtc aca    5236
Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr
                               100

gaa aag cat ctt acg gat ggc atg aca gta aga gaa tta tgc agt gct    5284
Glu Lys His Leu Thr Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala
            110                                      120

gcc ata acc atg agt gat aac act gcg gcc aac tta ctt ctg aca acg    5332
Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr
                           130

atc gga gga ccg aag gag cta acc gct ttt ttg cac aac atg ggg gat    5380
Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp
140                                          150

cat gta act cgc ctt gat cgt tgg gaa ccg gag ctg aat gaa gcc ata    5428
His Val Thr Arg Leu Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile
                       160                                      170

cca aac gac gag cgt gac acc acg atg cct gta gca atg gca aca acg    5476
Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Val Ala Met Ala Thr Thr
                               180

ttg cgc aaa cta tta act ggc gaa cta ctt act cta gct tcc cgg caa    5524
Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln
            190                                      100

caa tta ata gac tgg atg gag gcg gat aaa gtt gca gga cca ctt ctg    5572
Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu
                       110

cgc tcg gcc ctt ccg gct ggc tgg ttt att gct gat aaa tct gga gcc    5620
Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala
120                                      130

ggt gag cgt ggg tct cgc ggt atc att gca gca ctg ggg cca gat ggt    5668
Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly
                   140                                        150
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aag ccc tcc cgt atc gta gtt atc tac acg acg ggg agt cag gca act    5716
Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr
                            160

atg gat gaa cga aat aga cag atc gct gag ata ggt gcc tca ctg att    5764
Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile Gly Ala Ser Leu Ile
        170                                     180

aag cat tgg taa ctgtcagacc aagtttactc atatatactt tagattgatt       5816
Lys His Trp
    185

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Asn Ala Leu Ile Val Ile Leu Gly Thr Val Thr Leu Asp Ala Val Gly
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Arg Phe Gly Arg Arg Pro Val Leu Leu Ala Ser Leu Leu Gly Ala Thr
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Gly Ala Tyr Ile Ala Asp Ile Thr Asp Gly Glu Asp Arg Ala Arg His
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Phe Gly Leu Met Ser Ala Cys Phe Gly Val Gly Met Val Ala Gly Pro
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Val Ala Gly Gly Leu Leu Gly Ala Ile Ser Leu His Ala Pro Phe Leu
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Phe Asn Pro Val Ser Ser Phe Arg Trp Ala Arg Gly Met Thr Ile Val
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